BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

3-27-02

Express Mail No. EL 452 482 635 US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Sobek *et al.*

Group Art Unit: 1635

Serial No. 09/803,165

Examiner: Nguyen, L.

Filing Date: March 9, 2001

Attorney Docket No.: 5328

For: MUTANT B-TYPE POLYMERASES
IMPROVED PERFORMANCE IN PCR

COMMUNICATION

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Applicants submit herewith a certified copy of European Patent Application No. 00105155.6.

Applicant believes that no fee is due with this paper. However, if it is determined that a fee is due, please charge the required fee to Pennie & Edmonds LLP Deposit Account No. 16-1150 (order no. 1803-280-999).

Respectfully submitted,

Dated: March 14, 2002

42,983
Rahul Pathak (Reg. No.)

For: Jennifer Gordon (Reg. No. 30,753)
Pennie & Edmonds LLP
1155 Avenue of the Americas
New York, New York 10036
(212) 790-9090

Europäisches Patentamt	European Patent Office	Office européen des brevets

Bescheinigung Certificate Attestation

Die angehefteten Unterlagen stimmen mit der ursprünglich eingereichten Fassung der auf dem nächsten Blatt bezeichneten europäischen Patentanmeldung überein.

The attached documents are exact copies of the European patent application described on the following page, as originally filed.

Les documents fixés à cette attestation sont conformes à la version initialement déposée de la demande de brevet européen spécifiée à la page suivante.

Patentanmeldung Nr. Patent application No. Demande de brevet n°

00105155.6

Der Präsident des Europäischen Patentamts;
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
p.o.

I.L.C. HATTEN-HECKMAN

DEN HAAG, DEN
THE HAGUE, 27/11/00
LA HAYE, LE

Eur päisches Patentamt
European Patent Office
Office européen des brevets

Blatt 2 der Bescheinigung
Sheet 2 of the certificate
Page 2 de l'attestation

Anmeldung Nr.:
Application no.: 00105155.6
Demande n°:

Anmeldetag:
Date of filing: 11/03/00
Date de dépôt:

Anmelder:
Applicant(s):
Demandeur(s):
Roche Diagnostics GmbH
68298 Mannheim
GERMANY

Bezeichnung der Erfindung:
Title of the invention:
Titre de l'invention:
Mutant B-type DNA polymerases exhibiting improved performance in PCR

In Anspruch genommene Priorität(en) / Priority(ies) claimed / Priorité(s) revendiquée(s)

Staat: State: Pays:	Tag: Date: Date:	Aktenzeichen: File no. Numéro de dépôt:

Internationale Patentklassifikation:
International Patent classification:
Classification internationale des brevets:
C12N15/52, C12N9/00

Am Anmeldetag benannte Vertragstaaten:
Contracting states designated at date of filing: AT/BE/CH/CY/DE/DK/ES/FI/FR/GB/GR/IE/IT/LI/LU/MC/NL/PT/SE/TR
Etats contractants désignés lors du depôt:

Bemerkungen:
Remarks:
Remarques:

Roche Diagnostics GmbH

328/00/EP

Mutant B-type DNA polymerases exhibiting improved performance in PCR

FIELD OF THE INVENTION

Subject of the invention is a thermostable mutant B-type DNA-polymerase having a Y-GG/A amino acid motif between the N-terminal 3'-5'-exonuclease domain and the C-terminal polymerase domain in the wild type form whereas amino acids of this motif are substituted in the mutant form of the DNA polymerase and whereas these mutant DNA polymerases are suitable for PCR reactions. Thermostable mutants according to the present invention exhibit better performance in PCR reactions compared to the wild type DNA polymerase. A further embodiment of the present invention is the use of these thermostable mutants of the B-type DNA polymerase for polymerase chain reactions (PCR) and other nucleic acid synthesizing reactions. Another subject of the present invention is a method of producing the inventive mutants, vectors and cell lines comprising genes encoding the inventive mutants.

BACKGROUND OF THE INVENTION

DNA-dependent DNA polymerases containing proof-reading activity have to coordinate two catalytic activities: the DNA polymerase activity and the exonuclease activity. For polymerase I type DNA polymerases (*E. coli* Pol I) as well as for B-type DNA polymerases, these catalytic activities are located on structurally distinct protein domains (Truniger, V., Lázaro, J., Salas, M. and Blanco, L. (1996) *EMBO J.*, 15(13), 3430-3441; Pisani, F. M., De Felice, M. and Rossi, M. (1998) *Biochemistry*, 37(42), 15005-15012). In B-type (eukaryotic-type) DNA polymerases, the coordination of the two catalytic activities was proposed to take place intramolecularly in the conserved motif Y-GG/A located between the N-terminal 3'-5' exonuclease and the C-terminal polymerization domain (Truniger, V., Lázaro, J., Salas, M. and Blanco, L. (1996) *EMBO J.*, 15(13), 3430-3441; Pisani, F. M., De Felice, M. and Rossi, M. (1998) *Biochemistry*, 37(42), 15005-15012). For the Klenow fragment of *E.coli* DNA polymerase it was described, that the editing can

be an intermolecular or intramolecular process involving dissociation and reassociation of the DNA depending on the local context (Joyce, C. M. (1989) *JBC*, 264(18), 10858-10866). Truniger et al. (Truniger, V., Lázaro, J., Salas, M. and Blanco, L. (1996) *EMBO J.*, 15(13), 3430-3441) demonstrated for the mesophile replicative DNA polymerase of bacteriophage ϕ29 that mutations in the Y-GG/A motif can lead to phenotypes favoring either polymerisation or exonucleolysis compared to the wild type enzyme. They could show that this effect is related to altered (ss)DNA binding parameters and that the motif is important for the communication between the polymerase and exonuclease active site in a combination of structural and functional roles.

For the DNA polymerase of the thermophilic crenarchaeon *Sulfolobus solfataricus* (*Sso*) a region of 70 amino acids (region 1) involved in enzyme-DNA interaction was determined (Pisani, F. M., Manco, G., Carratore, V. and Rossi, M. (1996) *Biochemistry*, 35, 9158-9166). It is located in the connecting part between the exonuclease domain and the polymerase domain and contains the Y-GG/A motif. By mutational analysis of the amino acids in the Y-GG/A motif, it could be shown that the amino acids in this part of the enzyme determine the processivity of the proofreading function (Pisani, F. M., De Felice, M. and Rossi, M. (1998) *Biochemistry*, 37(42), 15005-15012). Based on the crystal structure of bacteriophage RB69 DNA polymerase, Truniger et al. proposed a direct interaction of the tyrosine with the phosphodiester bond between the two nucleotides preceding the one acting as template (Truniger, V., Blanco, L. and Salas, M. (1999) *J. Mol. Biol.*, 286, 57-69).

DESCRIPTION OF THE INVENTION

The subject of the present invention was to provide thermostable DNA polymerases exhibiting an improved performance in PCR. Especially, thermostable mutants of a B-type DNA polymerase are provided which exhibit improved PCR performance. The inventive mutants of the B-type DNA polymerase have mutations in the Y-GG/A amino acid motif. Preferred mutations refer to the position of the tyrosine in the Y-GG/A amino acid motif. Other mutations affecting the motif could also influence the performance of B-type DNA polymerases in PCR.

According to the present invention an improved performance of a DNA polymerase in PCR is defined as a performance that results in higher yields of PCR product, or the amplification of

longer DNA targets. Additionally, improved PCR performance can be defined as improved fidelity during the amplification process.

Preferred mutant B-type DNA polymerases have mutations at the position of the tyrosine in the Y-GG/A amino acid motif. Preferred mutants of B-type DNA polymerases according to the present invention have phenylalanine, tryptophan or histidine at the position of the tyrosine. Other preferred mutants of B-type DNA polymerases according to the present invention have asparagine or serine at the position of the tyrosine. These mutant polymerases described here, in which the tyrosine of the Y-GG/A motif was substituted, exhibit an improved performance in PCR.

In a preferred embodiment the inventive mutant B-type DNA polymerase is a mutant of a B-type DNA polymerase obtainable from Euryarchaea, more preferrably from *Thermococcus aggregans* (*Tag*). Especially preferred is a mutant of a B-type DNA polymerase from *Tag* of about 94 kDa size with a temperature optimum of $\geq$80° C and the ability to perform polymerase chain reactions.

The present invention is described in detail for the B-type DNA polymerase from *Thermococcus aggregans*, but the invention could also be applied to other B-type DNA polymerases. Preferrably to those B-type DNA polymerases showing a high degree of homology ($\geq$80%) to the DNA polymerase from *Thermococcus aggregans.*
The B-type DNA polymerase from *Thermococcus aggregans* exhibits a high degree of amino acid sequence homology to B-type DNA polymerases of other *Thermococcus* species. The homology of the DNA polymerases was calculated using the programm Blast 2 (Tatusova, T.A. and Madden, T.L. (1999) *FEMS Microbiol. Lett.* 174, 247 – 250). The homology of the B-type DNA polymerase from *Thermococcus aggregans* to the homologue enzymes from *Thermococcus* species is: 93% (*T. litoralis*), 87% (*T. gorgonarius*), 86% (*T. furiosus*) and 87% (*T.* spec. 9N7). The homology of the *Tag* DNA polymerase to polymerases from *Pyrococcus* species is: 86% (*P. abysii*), 86% (*P. horikoshii*), 86% (*P.* spec KOD) and 85% (*P. furiosus*). A lower homology is calculated to other B-type DNA polymerase from different euryarchaeota: 59% (*Methanococcus jannaschii*), 56% (*Methanococcus voltae*), 51% (*Methanobacterium thermoautotrophicum*) and 56% (*Archaeglobus fulgidus*). To B-type DNA polymerases from crenarchaeota and bacteriophages the homology is found as follows: 46% (*Sulfolobus solfataricus*), 42% (*Sulfolobus acidocaldarius*), 41% (*Sulfurisphera ohwakuensis*), 51% (*Aeropyrum pernix*), 40% (*Pyrodictium occultum*), 43% (*Cenarchaeum symbiosum*), 38% (bacteriophage T4) and 39% (bacteriophage RB69).

As described above several mutations in the Y-GG/A motif were performed for the *Sulfolobus solfataricus* (*Sso*) and the ϕ29 DNA polymerases. The observed effects on polymerase activity (pol) and exonuclease activity (exo) of these mutations do not completely correspond to the effects obtained for the *Tag* DNA polymerase. Thus the effect of the mutations on the performance of the mutants in PCR was not predictable.
The mutant Y387F of the *Tag* DNA polymerase exhibits a higher pol/exo ratio compared to the wild type *Tag* DNA polymerase. Similar results were described for *Sso* and ϕ29 DNA polymerase. The mutant G389A displays the opposite effect than the corresponding mutant in ϕ29 DNA polymerase: while G→A in *Tag* DNA polymerase almost knocks out polymerase activity, in ϕ29 DNA polymerase G→A mutant this activity is clearly enhanced. For mutants of the *Sso* DNA polymerase a change of exonuclease processivity was described. Again, this was not observed for mutants of the B-type *Tag* DNA polymerases. Thus, a prediction of the effect of analogous mutants in the Y-GG/A motif could not be made.

In summary, although it has been described in the prior art that the Y-GG/A motif plays a role in the coordination of the DNA polymerase activity and the exonuclease activity, the observed changes of the pol/exo ratio of the prior art DNA polymerases do not strictly correlate to the changes observed for the inventive mutants of the *Tag* DNA polymerase. Furthermore, it has not been described that the Y-GG/A motif is important for the performance of B-type DNA polymerase in PCR. Additionally, there is no correlation between the changes of the pol/exo ratio and the improvement of the performance of DNA polymerases in PCR. For instance, the mutant Y387H does not exhibit a change of pol/exo ratio compared to the wild-type, but it exhibits improved performance in PCR. Furthermore, a significant enhancement of fidelity was observed for the mutants Y387N and Y387S of *Tag* DNA polymerase.

Results obtained for the mutants of *Tag* DNA polymerase are described in more detail below.

Enzymatic activities of wild type and mutant *Tag* DNA polymerases

The enzymatic activities of the wild type enzyme and the mutants of *Tag* DNA polymerase were determined and analyzed (Figure 1). The DNA polymerase activity was determined as described in Example 2. According to the effect of the mutations on the polymerase activity three groups of

mutants were defined: i) mutants with enhanced DNA polymerase activity (mutant Y387F), ii) mutants having a similar or slighlty reduced DNA polymerase activity compared to the wild type (mutants Y387W and Y387H) and iii) mutants with reduced DNA polymerase activity (mutants Y387N, Y387S, G389A).
The exonuclease activity was determined as described in Example 3. According to the effect of the mutations on the exonuclease activity two groups of mutants were defined: i) mutants with similar exonucleolytic activity as the wild type enzyme (mutants Y387F, Y387W, Y387H), ii) mutants with enhanced exonuclease activity (mutants Y387N, Y387S, G389A) in comparison to the wild type enzyme.

From the data obtained for polymerase activity and exonuclease activity the ratios of both activities (pol/exo) were calculated for the wild type enzyme and the mutants of *Tag* DNA polymerase (Figure 1). Three mutants showed a higher or similar pol/exo ratio as the wild type enzyme (mutants Y387F, Y387W, Y387H). Three mutants showed a clearly reduced pol/exo ratio in comparison to the wild type enzyme (mutants Y387N, Y387S, G389A).

PCR performance

Wild type and mutant enzymes were submitted to polymerase chain reactions on lambda DNA in a buffer optimized for this purpose. All mutants except for mutant G389A were able to perform PCR, but yielded different amounts of product with a constant amount of enzyme (1 pmol). With increasing length of the DNA target, differences in performance of the enzyme were shown (Fig. 2). With 1 pmol of the mutants Y387S, Y387N and G389A no PCR product could be obtained for the amplification of a 3.3 kb fragment. 1 pmol of the wild type DNA polymerase could not amplify fragments of 5.0 kb length. The mutants Y387W, Y387F and Y387H were able to amplify a fragment of 7.5 kb length. As control *Taq* DNA polymerase, *Pwo* DNA polymerase and Expand^{TM} High Fidelity PCR System (Roche Molecular Biochemicals) were used.

The differences in PCR performance were also shown by the amplification of a 2 kb fragment applying different elongation times in the PCR runs. Under these conditions, all enzymes tested except the mutant G389A were able to amplify a 2 kb fragment at an elongation time of 90 sec/cycle. The mutants Y387F, Y387W and Y387H were able to amplify the fragment at a reduced elongation time of 40 sec/cycle. The mutant Y387H was able to amplify the target in a elongation time of 30 sec/cycle (Fig. 3).

Exonuclease processivity

The exonuclease processivity of the enzymes was studied in an experiment based on the heparin trap method (Reddy, M. K., Weitzel, S. E. and von Hippel, P. H. (1992) *J. Biol. Chem.*, 267(20), 14157-14166; Pisani, F. M., De Felice, M. and Rossi, M. (1998) *Biochemistry*, 37(42), 15005-15012). A constant amount (1 pmol) of *Tag* DNA polymerase or its mutants was incubated for 4 minutes at 68 °C with a 5'-DIG-labelled 24mer oligonucleotide in the absence of nucleotides. In the absence of heparin, the oligonucleotide was continually degraded by the *Tag* enzymes (positive control, Fig. 4, lanes "-"). The function of the heparin trap method was demonstrated by addition of heparin and $MnCl_2$ before the binding of the enzyme (negative control, Figure 4, lanes B). Single turnover conditions (addition of heparin and $MnCl_2$ to start the reaction after the binding of enzyme) resulted in exonucleolytic degradation of the oligonucleotide by the *Tag* DNA polymerases (Fig. 4, lanes A). The enzymes showed differences in the exonucleolytic activity as shown by the different amounts of remaining oligonucleotide that was not degraded. However, for all enzymes tested the oligonucleotide was degraded to a similar extent (8 nt). This indicates a similar exonuclease processivity for the enzymes.
The *Thermococcus gorgonarius* DNA polymerase, which exhibits a strong exonuclease activity, was used as a positive control. It degraded the 24mer oligonucleotide in the absence of heparin to oligonucleotides of less than 15 bases length (Figure 4, lane "-"). Under single turnover conditions a strong degradation (11 nt) of the oligonucleotide is observed (Figure 4, lane "A").

Fidelity

The error rates in amplification were determined for the mutant enzymes and the wild type DNA polymerase. The PCR-based fidelity assay described by Frey and Suppman (Frey, M. and Suppmann, B. (1995) *Biochemica*, 2, 34-35) was used. This method is based on the amplification, circulation and transformation of the pUC19 derivative pUCQ17, which contains a functional *lacI*^{q} allele (Barnes, W. M. (1994) *Proc. Natl. Acad. Sci. USA*, 91, 2216-2220). PCR-derived mutations in *lacI* result in a de-repression of the expression of *lacZ*α and subsequent formation of a functional β-galactosidase enzyme, which can be detected on X-Gal indicator plates.

In five independent runs, a mean error rate of 5.0×10^{-6} was found for the wild type *Tag* DNA polymerase. This value is in between the mean error rates of 1.8×10^{-6} for Expand^{TM}High Fidelity PCR System (Roche Molecular Biochemicals) and 1.3×10^{-5} for *Taq* DNA polymerase

(Roche Molecular Biochemicals) determined in the corresponding experiments. For a better comparison of the data, we plotted the quotient of the error rate determined for *Taq* DNA polymerase divided by the error rates determined for the *Tag*
DNA polymerase and its mutants. In the independent experiments the error rate for *Taq* DNA polymerase varied from 1.2 to 3.05×10^{-5}.
Figure 5 shows the quotients of the error rates of the wild type enzyme and mutants of *Tag* DNA polymerase. The error rates of the mutants showing improved PCR performance (Y387W, Y387F, Y387H) did not significantly differ from the values obtained for the wild type enzyme. The mutants with enhanced exonuclease activity (Y387N, Y387S) showed improved fidelity rates (Figure 5). For the mutants Y387N and Y387S mean error rates of 6.3×10^{-7} and 6.2×10^{-7} were determined.

In contrast to the ϕ29 DNA polymerase and the *Sso* DNA polymerase, the *Tag* DNA polymerase, is suited for PCR. The mutant enzymes (Y387F, Y387W, Y387H) with an aromatic amino acid in the position of the tyrosine showed a similar or only slightly enhanced DNA polymerase activity (mutants Y387F, Y387W, Y387H) but an improvement in PCR performance.

In the fidelity assay it was found that the mutants Y387F; Y387W and Y387H showed no significant change in their error rate. By contrast, the mutants Y387N or Y387S showed higher exonuclease activity and displayed an improved fidelity.

Subject of the present invention is also a method of producing the inventive B-type mutants comprising the following steps: cloning and mutagenesis of the gene, followed by the expression and purification of the protein.

Subject of the present invention is a DNA encoding for a thermostable B-type DNA polymerase having a Y-GG/A amino acid motif between the N-terminal 3'-5' exonuclease domain and the C-terminal polymerase domain in the wild type enzyme whereas the tyrosine of this motif is substituted in the mutant enzyme of the polymerase and whereas this mutant DNA polymerase is suitable for PCR.

Preferably, said DNA in wild type form is obtainable from Euryarchaea, more preferably from *Thermococcus aggregans* (*Tag*). Subject of the present invention is also a vector containing the inventive DNA. Suitable vectors are e.g. the following: pET14b/15b/16b/19b (Novagen); pRSET

(Invitrogen); pTrcHis (Invitrogen); pHAT10/11/12 (Clontech); pPRO Tet.E/Lar.A (Clontech); pCALn/n-EK (Stratagene); pGEMEX-1/-2 (Promega).

Furthermore, subjects of the present invention are also cells comprising the above vector. Suitable cells are e.g. *E.coli* BL21, BL21(DE3), BL21(DE3)pLysS, BL21(DE3)pLysE, DH5∝PRO, JM109 (DE3), TOP10 in combination with the vectors recommended by the suppliers. The gene may have to be subcloned and the protein purification procedure may have to be adapted in the case of different expression vectors.
A sample of the recombinant strain expressing *Tag* DNA polymerase was deposited with the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) Mascheroder Weg 1b, D-38124 Braunschweig (DSM No. 13224).

A further subject of the invention is the use of the inventive mutant enzymes for synthesizing nucleic acids e.g. in PCR reactions.

DETAILED DESCRIPTION OF THE PREFERED EMBODIMENTS

Figures:

Figure 1.

Table showing the relative polymerase activities (Pol) and 3'-5'-exonuclease activities (Exo) of *Tag* DNA polymerase and its mutants on double-stranded DNA.

Assays were carried out as described in example 2 and 3, respectiviely. The activites are expressed as percentage of the activity obtained for the wild-type *Tag* DNA polymerase.

Figure 2.

PCR with *Tag* DNA polymerase mutants.

Tag DNA polymerase mutants (1 pmol) were incubated in a 50 µl total volume with 10 ng of lambda DNA as template and 30 pmoles of a primer set designed to yield the indicated fragment lengths, 200 µM dNTPs and the suitable PCR buffer. Reactions were performed with 10 cycles of 10 sec 94 °C, 30 sec 57 °C and 3.0 min (A), 4.3 min (B) or 7.0 (C) min of elongation time at 72 °C followed by 20 cycles with elongation times increasing by 20 sec/cycle. After the PCR 5 µl sample were submitted to electrophoresis on a 1% agarose gel. For the control reaction 2.5 U of *Taq* DNA polymerase, *Pwo* DNA polymerase or Expand™ High Fidelity PCR System were used. The labeling of the lanes is described in the legend of figure 6.

Figure 3.

Time-dependent polymerase chain reaction.

1% agarose gels showing 2 kb PCR products from reactions performed with different elongation time (90 sec, 40 sec, 30 sec as indicated) to determine the minimal elongation time.

1 pmol of each *Tag* DNA polymerase mutant or wild type enzyme was added to a mix of 10 ng lambda DNA and primers designed to yield 2 kb DNA fragments. Labeling of the lanes is described in the legend of figure 6. For each mutant duplicate reactions were performed. Right lane of each gel *Pwo*: 2.5 U *Pyrococcus woesei* DNA polymerase (Roche Molecular Biochemicals) as control reaction. Left lane of each gel: Molecular weight marker VI (Roche Molecular Biochemicals). In the 40 sec reaction, mutant GA was omitted. In the 30 sec reaction, for the mutant YS only one reaction was run on the gel.

Figure 4.

3'-5'-exonuclease processivity.

The *Tag* DNA polymerase mutants tested are indicated on top of the figure. *Tgo* DNA polymerase was used as a control reaction (incubation for 30 sec). Reactions for wild type and mutants of *Tag* DNA polymerase were performed for 4 minutes at 68 °C after preincubation for 1 minute at 68°C. Lane "P" is the control reaction (24 mer 5'-DIG-labelled primer without incubation), lane "-": reaction without heparin (positive control); lane "B": reaction with heparin and $MnCl_2$ added before addition of the enzyme (negative control); lane "A": heparin and $MnCl_2$ added after the enzyme (reaction under single turnover conditions).

Figure 5.

Fidelity of *Tag* DNA polymerase mutants.

The fidelity of *Tag* DNA polymerase and its mutants was expressed in relation to the fidelity of *Taq* DNA polymerase. A quotient of 1 means that the polymerase has the same error rate as *Taq* DNA polymerase (mean value $1.3x10^{-5}$). Values >1 reflect the factor by which a polymerase shows less errors than *Taq* DNA polymerase. The bars correspond to to mean values calculated from 2-5 independent experiments, error bars missing are smaller than 0.36. Abbreviations for enzymes are as indicated in legend to figure 6. As controls *Pyrococcus woesei* DNA polymerase (Roche Molecular Biochemicals) and Expand High Fidelity PCR System (Roche Molecular Biochemicals) were used („Taq/Pwo" and „Taq/HiFi").

Figure 6.

SDS-PAGE gel analysis of purified mutant proteins.

1 µg of each mutant was submitted to electrophoresis on an 10% SDS-PAGE gel. Left: MW, molecular weight marker; WT, *Thermococcus aggregans* wild type DNA polymerase; YF, YW, YS, YN, YH are the corresponding mutants with an exchange at the position of tyrosine 387 to phenylalanine, tryptophan, serine, asparagine, histidine, respectively. GA, mutation of glycine 389 to alanine in the gene of the *Thermococcus aggregans* DNA polymerase. All mutants showed the same chromatographic behaviour and solubility as the wild type enzyme.

Figure 7.

Qualitative exonuclease assay.

A DNA molecular weight marker was used as substrate to test the exonucleolytic activity (DNA molecular weight marker II (MW II), Roche Molecular Biochemicals). 1 µg of MW II was incubated for 6 h at 65 °C with 1 pmol of each variant of *Tag* DNA polymerase in the presence (A) or absence (B) of 200 µM dNTP. *Tag* mutants are named as explained in legend of figure 6. Exonucleolytic degradation take place only in the absence of deoxynucleotides. The qualitative ranking of the proteins in terms of exonuclease activity is GA > YN > YS > YH > YF = YW = WT.

Figure 8.

Consensus sequence motif for B-type DNA polymerases from the order of *Thermococcales* derived from a multiple alignment of amino acid sequences of euryarchaeal and crenarchaeal B-type DNA polymerases.

A region of 24 amino acids containing the Y-GG/A motif was analyzed with the ClustalW Software program (Higgins, EMBL Heidelberg, Germany). In addition to the amino acids conserved in all archaeal B-type DNA polymerases (like the Y-GG/A motif), a consensus sequence "E--RR-R-----G(Y)-KE-EE--LWE-" can be defined. This sequence is found in the sequence of all DNA polymerases belonging to the order of the *Thermococcales* and coincides with a homology of >80% of the DNA polymerases.

The sequences of the crenarchaeal species *Sulfolobus solfataricus*, *Sulfolobus acidocaldarius*, *Pyrobaculum islandicum*, *Pyrodictium occultum*, *Aeropyrum pernix*, *Sulfurisphaera ohwakuensis* and the sequences of several euryarchaeal species *Thermococcus* ("T."), *Pyrococcus* ("P.") and *Methanococcus* ("M.") were aligned.

Figure 9.

DNA sequence and deduced amino acid sequence of recombinant wild type *Tag* DNA polymerase.

Three inteins found in the native gene (Acc. No. Y13030) were deleted by PCR (Niehaus, F., Frey, B., Antranikian, A. (1997) *Gene*, 204, 153-158). Four mutations leading to amino acid exchanges were introduced during PCR. The amino acid exchanges (native→recombinant) are: L3F, A404T, S410C and L492H.

Example 1

Site-directed mutagenesis and expression of *Tag* DNA polymerase mutants

The cloning of the gene of *Tag* DNA Polymerase (polTY) was described earlier (Niehaus, F., Frey, B., Antranikian, A. (1997) *Gene*, 204, 153-158). Overexpression of *Tag* DNA Polymerase in *E. coli* was achieved by subcloning its encoding gene into the IPTG-inducible pET15b vector (Novagen) containing an N-terminal His-Tag for purification (the resulting plasmid was named pET15b-TagPol).

The mutants presented in this study were prepared in polymerase chain reactions using primers containing the desired mutations as a mismatch. The forward primer was universally "Kpn-fw", matching to a sequence about 100 bp upstream of the mutation site and contained a *Kpn*I restriction site of the polTy gene. The reverse primers contained a *Sna*BI restrition site and additionally the desired mutation. The sequences of the oligonucleotides were as follows (mismatch sites for mutagenesis underlined):

Kpn-Fw 5'-GCAACCTTGTAGAGTAGAGTGGTACCTGTTAAGGG-3';
TagY387F 5'-GCCTCTTTCCGGCTCTTTTACGTATCCTCCCAGGAAAGTAGTCC-3',
TagY387H 5'-GCCTCTTTCCGGCTCTTTTACGTATCCTCCCAGGTGAGTAGTCC-3',
TagY387N 5'-GCCTCTTTCCGGCTCTTTTACGTATCCTCCCAGGTTAGTAGTCC-3',
TagY387S 5'-GCCTCTTTCCGGCTCTTTTACGTATCCTCCCAGGGAAGTAGTCC-3',
TagY387W 5'-GCCTCTTTCCGGCTCTTTTACGTATCCTCCCAGCCAAGTAGTCC-3',
TagG389A 5'-GCCTCTTTCCGGCTCTTTTACGTATCCAGCCAGGTAAGTAGTCC-3'.

PCR reactions were carried out with Expand^{TM} High Fidelity PCR System (Roche Molecular Biochemicals) using the following program: 2 min 94 °C, 30 cycles of 10 sec 94 °C, 30 sec 55 °C, 30 sec at 72 °C. The resulting 139 bp fragments were digested with the restriction enzymes *Kpn*I and *Sna*BI yielding a 101 bp fragment that was ligated into pET15b-TagPol linearized with the restriction enzymes *Kpn*I and *Sna*BI. The cloned DNA fragments were sequenced to confirm the presence of the desired mutations.

For protein expression, *E. coli* BL21 (DE3) cells were transformed with the expression vector pET15b-TagPol. Three to five colonies were inoculated in 15 ml of LB medium supplemented with 100 µg Ampicillin per ml and grown to OD_{600nm} 0.3. An aliquot (10 ml) of the preculture was used to inoculate 500 ml of LB medium and incubated while shaking at 37°C. At OD_{600nm}= 0.6 expression was induced by addition of IPTG (final concentration: 1 mM). After incubation

for 3 hours cells were harvested by centrifugation and suspended in 50 mM Tris-HCl/pH 7.5, 10 mM KCl, 0.5 mM EDTA, 4 mM $MgCl_2$, 5 mM DTT. Cells were sonicated on ice and the crude extract was heated for 15 min to 80 °C. Cell debris was removed by centrifugation (30 min, 30 000 x g at 4 °C).

The supernatant was applied to a Blue Sepharose 3G-A column (Pharmacia) equilibrated with buffer A (50 mM Tris-HCl/ pH 7.5, 10 mM KCl, 4 mM Mg Cl_2). The protein was eluted with a gradient of 0.01-1.5 M KCl. Active fractions were pooled and dialyzed against 20 mM Tris-HCl /pH 7.9, 5 mM imidazole, 500 mM NaCl. The sample was applied to a Ni-chelate column (Novagene) equilibrated in the same buffer and eluted with a gradient of 0.005 - 1 M imidazole. Active fractions were pooled and dialyzed against storage buffer (50 mM Tris-HCl/pH 7.5, 100 mM KCl, 0.5 mM EDTA, 5 mM DTT, 50% glycerol). The enzymes were pure as shown by SDS gel electrophoresis (Figure 6).

Example 2

DNA polymerase assay

The DNA polymerase activity was determined by measuring the incorporation of α-(^{32}P)dCTP in a DNA substrate. The test mix (50 µl) contained 5 µl 10x *Tag* reaction buffer (100 mM Tris-HCl /pH 8.9, 750 mM KCl, 15 MgCl2, 100 mM CHAPS), 200 µM of each dATP, dGTP, dTTP, 100 µM dCTP, 1 mCi α-(^{32}P)dCTP, 1 µg of M13mp9 ssDNA annealed with 0.3 µg M13 primer. Assays were performed with 2 and 3 µl of enzyme in three different dilutions (final amount of enzyme 2.5 to 15 fmoles) yielding six reactions to calculate a mean value. As a reference *Pwo* DNA polymerase was used. The DNA/primer mix was prepared by heating 277.2 µg M13mp9 ssDNA (Roche Molecular Biochemicals) and 156 µg M13 sequencing primer (17mer forward primer, Roche Molecular Biochemicals) for 30 minutes to 55 °C and then cooling it for 30 minutes to room temperature.

Assay reactions were incubated for 30 minutes at 65 °C, stopped on ice by addition of 500 µl of 10% TCA (4 °C) and kept on ice for another 10 minutes. Samples were filtered over GFC-filter (Whatman), filters washed three times with 5% TCA, dried and submitted to β-counting in 2 ml of scintillation fluid. One unit is defined as the amount of enzyme necessary to incorporate 10 nM dNTP into acid insoluble material at 65 °C in 30 minutes.

Example 3

Exonuclease Assays

Activity Assay

3 µl (300 ng) of enzyme (approximately 5 Units of polymerase activity) were incubated with 5 µg of 3H-labelled calf thymus DNA for 4 hours at 65 °C in a buffer containing 10 mM Tris-HCl/pH 8.9, 75 mM KCl, 1.5 $MgCl_2$, 10 mM CHAPS. Radioactivity liberated from calf thymus DNA was measured in a scintilation counter.

The assay used does not discriminate between the 3'-5' exonuclease activity and the 5'-3' exonuclease activity. 5'-3'-exonuclease activity has not been detected pheno- or genotypically in B-type polymerases of *Thermococcales* (Perler, F. B., Kumar, S. and Kong, H. (1996) *Adv. Prot. Chem.*, 48, 377-435). Thus the values obtained can be regarded as 3'-5'-exonuclease activity.

In another assay, 1 µg of molecular weight marker II (Roche Molecular Biochemicals) were incubated in same buffer as above with 5 U of the indicated protein with or without 200 µM dNTP in a final volume of 50 µl for 6 hours at 65 °C. The reaction products were separated by electrophoresis on 1% agarose gels.

3'-5' Exonuclease processivity assay

The previously described heparin trap method was used (Reddy, M. K., Weitzel, S. E. and von Hippel, P. H. (1992) *J. Biol. Chem.*, 267(20), 14157-14166; Pisani, F. M., De Felice, M. and Rossi, M. (1998) *Biochemistry*, 37(42), 15005-15012). A reaction mix (10 µl) containing 10 mM Tris-HCl/pH 8.9, 75 mM KCl, 10 mM CHAPS and 0.5 pmoles of a 5'-DIG-labeled 24mer oligonucleotide was prewarmed for 1 minute at 68 °C in a thermocycler. Unless otherwise noted, 1 pmol of the enzyme was preincubated for 1 minute at 68 °C with the substrate. The reaction was started by addition of $MnCl_2$ (final concentration: 4 mM) and heparin (final concentration:1 mg/ml) to ensure single turnover conditions. After incubation for 4 minutes, the reaction was stopped by the addition of 5 µl of formamide buffer (80% formamide, 10 mM EDTA, 1 mg/ml bromophenol blue, 1 mg/ml xylene xyanol). The efficiency of the heparin trap was checked in a control reaction by adding heparin and $MnCl_2$ prior to the addition of the enzyme. The samples were denaturated for 3 minutes at 90 °C and subjected to denaturing gel electrophoresis on a 17.5 % polyacrylamide/8 M urea gel. Gels were blotted to a positively charged nylon membrane (Roche Molecular Biochemicals) and the blots developed with CPD-Star (Roche Molecular Biochemicals) according to the manufacturers instructions.

Example 4

*lac*I-based PCR fidelity assay

We used the *lac*I-based PCR fidelity assay described by Frey and Suppmann (Frey, M. and Suppmann, B. (1995) *Biochemica*, 2, 34-35). This method is based on the amplification, circularization and transformation of the pUC19 derivative pUCQ17, which contains a functional *lac*I^{q} allele (Barnes, W. M. (1994) *Proc. Natl. Acad. Sci. USA*, 91, 2216-2220). PCR-derived mutations in *lac*I result in a de-repression of the expression of *lacZ*α and subsequent formation of a functional β-galactosidase enzyme, which can be easily detected on X-Gal indicator plates.

The truncated *lac*I gene of pUC19 was substituted by a functional copy of *lac*I^{q}. A 178 bp *Pvu II-Afl III* fragment was replaced by a 1121 bp DNA fragment encoding *lac*I^{q}. The α-complementing *E. coli* strain DH5α, once transformed with the resulting plasmid pUCIQ17 (3632 bp), produces white (LACI^{+}) colonies on LB plates containing ampicillin (100 µg/ml) and X-Gal (0,004% w/v). For the PCR, pUCIQ17 was linearized by digestion with *Dra* II and used as a template in an amount of 1 or 10 ng. Both primers have *Cla* I cleavage sites at their 5' ends. Oligonucleotide Cla33 (34mer, 24 matches: 5'-AGC TTA TCG ATG GCA CTT TTC GGG GAA ATG TGC G-3') and Oligonucleotide Cla55 (36mer, 26 matches: 5'- AGC TTA TCG ATA AGC GGA TGC CGG GAG CAG ACA AGC-3') resulted in a PCR product of 3493 bp.
The reactions were performed with 1 or 5 pmol of protein in the *Tag* polymerase PCR buffer described below or for the control reactions in the manufacturers PCR buffers with 2.5 U of enzyme. The cycle conditions were 10 sec denaturation at 94 °C, 30 sec annealing at 57 °C and 4 min elongation at 72 °C for 18, 24 or 30 cycles depending on the enzyme.
After PCR, the yield of amplification product was determined at (OD_{260nm} or in agarose gel) and the DNA fragments submitted to phenol/chloroform extraction to eliminate any protein. After digestion with *ClaI*, the DNA fragments were purified from a preparative agarose gel. Ligation reactions were carried out with the Rapid Ligation Kit (Roche Molecular Biochemicals), the reactions contained 30 ng DNA. The resulting circular plasmids were transformed in *E. coli* DH5α as described by Hanahan (Hanahan, D. (1983) *J. Mol. Biol.*, 166, 557-580) and plated on LB Amp/X-Gal plates described above. After incubation overnight at 37 °C, blue and white colonies were counted. The error rate (f) per bp was calculated with a rearranged equation published by Keohavong and Thilly (Keohavong, P. and Thilly, W. G. (1989) *Proc. Natl. Acad. Sci. USA*, 86, 9253-9257): f = -lnF / d x b bp.

Where F is the fraction of white colonies (white colonies/ total colonies); d is the number of DNA duplications: 2^d = output DNA/input DNA and b is the effective target size (1080 bp) of the *lacI* gene. There are 349 phenotypically identified (by colour screening) single-base substitutions (non-sense and mis-sense) at 179 codons (approximately 50% of the coding region) within the *lacI* gene. (Provost, G. S., Kretz, P. L., Hamner, R. T., Matthews, C. D., Rogers, B. J., Lundberg, K. S., Dycaico, M. J. and Short, J. M. (1993) *Mut. research*, 288, 133-149). Frameshift errors which may occur at every position in the 1080 bp open reading frame of *lacI*, are not taken into account because little information is available for the specific polymerases used in PCR systems except for *Taq* DNA polymerase.

Example 5

Polymerase Chain Reactions

PCR was performed in a buffer optimized for *Tag* DNA polymerase and its mutants: 10 mM Tris-HCl/pH 8.9, 75 mM KCl, 1.5 $MgCl_2$, 10 mM CHAPS, 200 µM dNTP. 10 ng of λ DNA were used as a template and 30 pmol of each primer (20 bp, designed to yield the products of the desired length):
Lambda 1, universal forward primer: 5'-GAT GAG TTC GTG TCC GTA CAA CA-3',
Lambda 3.3: 5'-CTC ATC AGC AGA TCA TCT TCA GG-3',
Lambda 8: 5'-ACT CCA GCG TCT CAT CTT TAT GC-3',
Lambda 9: 5'-GAT GGT GAT CCT CTC TCG TTT GC-3'.
Lambda 3.3, 8 and 9 were used as reverse primers for the amplification of 3 kb, 3.5 kb and 7.5 kb fragments respectively.
Template, primers and nucleotides were prepared in mix 1 in a volume of 25 µl. Then 25 µl of mix 2 containing the buffer and enzyme (1 pmol *Tag* wild type or mutant; or 2.5 U control enzyme) were added. All reactions were prepared in duplicate. The amplification was performed in a 2400 GeneAmp thermocycler (Perkin Elmer). The cycle conditions were: 2 min at 94 °C, 10 cycles with 10 sec denaturation at 94 °C, 30 sec annealing at 58 °C and elongation at 72 °C. Elongation times depended on the length of the product (3 min for 3.3 kb, 4.3 min for 5 kb and 7 min for 7,5 kb). Another 20 cycles were performed with increasing the elongation times by 20 sec/cycle. The reaction was finished by 7 minutes at 72 °C. The tubes were kept at 4 °C until separation by electrophoresis on 1% agarose gels.

The improvement of the PCR performance of the mutants was also studied in a "time-dependent PCR". A 2 kb fragment was amplified from lambda DNA as described above. In these studies the

elongation time of the PCR was stepwise reduced (90 sec, 40 sec, 30 sec) to determine for each enzyme the minimal elongation time that was sufficient to amplify the 2 kb fragment. The following primers were used:

Lambda 1, universal forward primer: 5'-GAT GAG TTC GTG TCC GTA CAA CA-3',

Lambda 6, reverse primer: 5'-CTT CAT CAT CGA GAT AGC TGT CG-3'.

The temperature profile was as described above. The elongation times were kept constant over 30 cycles.

Claims

1. A thermostable mutant B-type DNA polymerase having a Y-GG/A amino acid motif between the N-terminal 3'-5'-exonuclease domain and the C-terminal polymerase domain in the wild-type form of the polymerase whereas preferrably the tyrosine of this motif is substituted in the mutant form of the polymerase and whereas this mutant DNA polymerase is suitable for polymerase chain reactions.

2. A mutant B-type DNA polymerase according to claim 1 having an amino acid with an aromatic side chain at the position of the tyrosine.

3. A mutant thermostable B-type DNA polymerase according to claim 1 having a Y→F,Y→W or Y→H mutation.

4. A mutant B-type DNA polymerase according to claim 1 having an amino acid with an hydrophilic side chain at the position of the tyrosine.

5. A mutant thermostable B-type DNA polymerase according to claim 1 having a Y→N or Y→S mutation.

6. A mutant thermostable B-type DNA polymerase according to claims 1-5 whereas the wild type form is obtainable from Euryarchaea.

7. A mutant thermostable B-type DNA polymerase according to claims 1-6 whereas the wild type form is obtainable from *Thermococcus aggregans*.

8. A mutant of a thermostable B-type DNA polymerase according to claims 1-6 whereas the amino acid sequence of the wild type form is ≥80% homologue to the amino acid sequence of wild type *Tag* DNA polymerase.

9. A DNA encoding a thermostable mutant DNA polymerase according to claims 1-8.

10. A vector containing a DNA according to claim 9.

11. A transformed host cell comprising a vector according to claim 10.

12. A process for obtaining a polymerase according to claim 1-8 comprising the steps of cloning and mutagenesis of the gene, followed by the expression and purification of the protein.

13. Use of a polymerase according to claim 1-8 for synthesizing nucleic acids.

14. Use of a polymerase according to claims 1-8 for PCR reactions.

Abstract

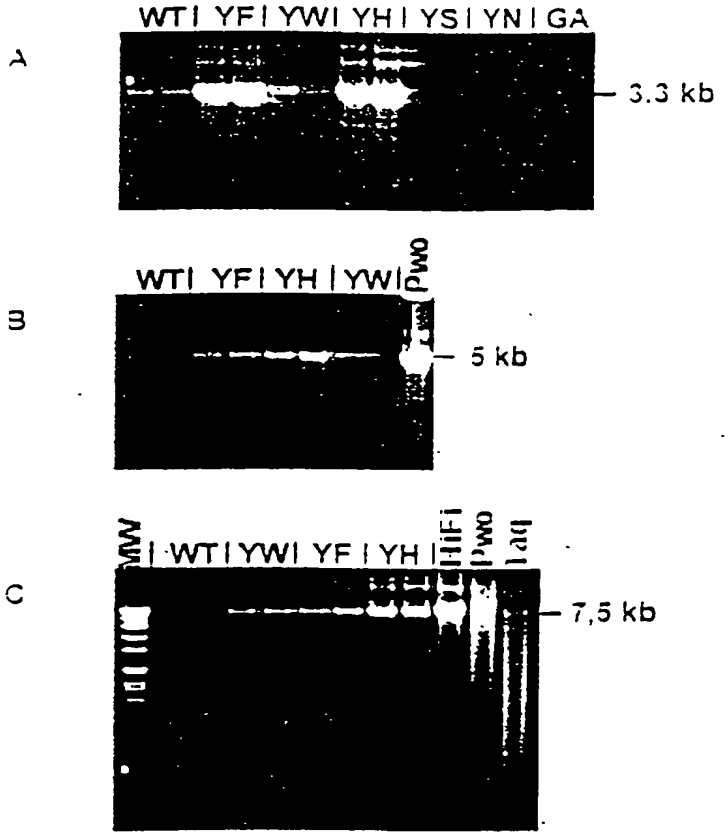
Claimed are thermostable mutants of B-type DNA polymerases having a Y-GG/A amino acid motif between the N-terminal 3'-5'-exonuclease domain and the C-terminal polymerase domain whereas the tyrosine of the Y-GG/A amino acid motif is mutated and whereas these mutant DNA polymerases are suitable for PCR.

Figure 1.

Pol activity and Exo activity in %

	WT	Y387F	Y387W	Y387H	Y387N	Y387S	G389A
Pol	100	160	92	93,6	6,4	17,8	10,7
Exo	100	90	71	98	205	187	236
Pol/Exo	1	1,77	1,29	0,96	0,03	0,09	0,04

Figure 2



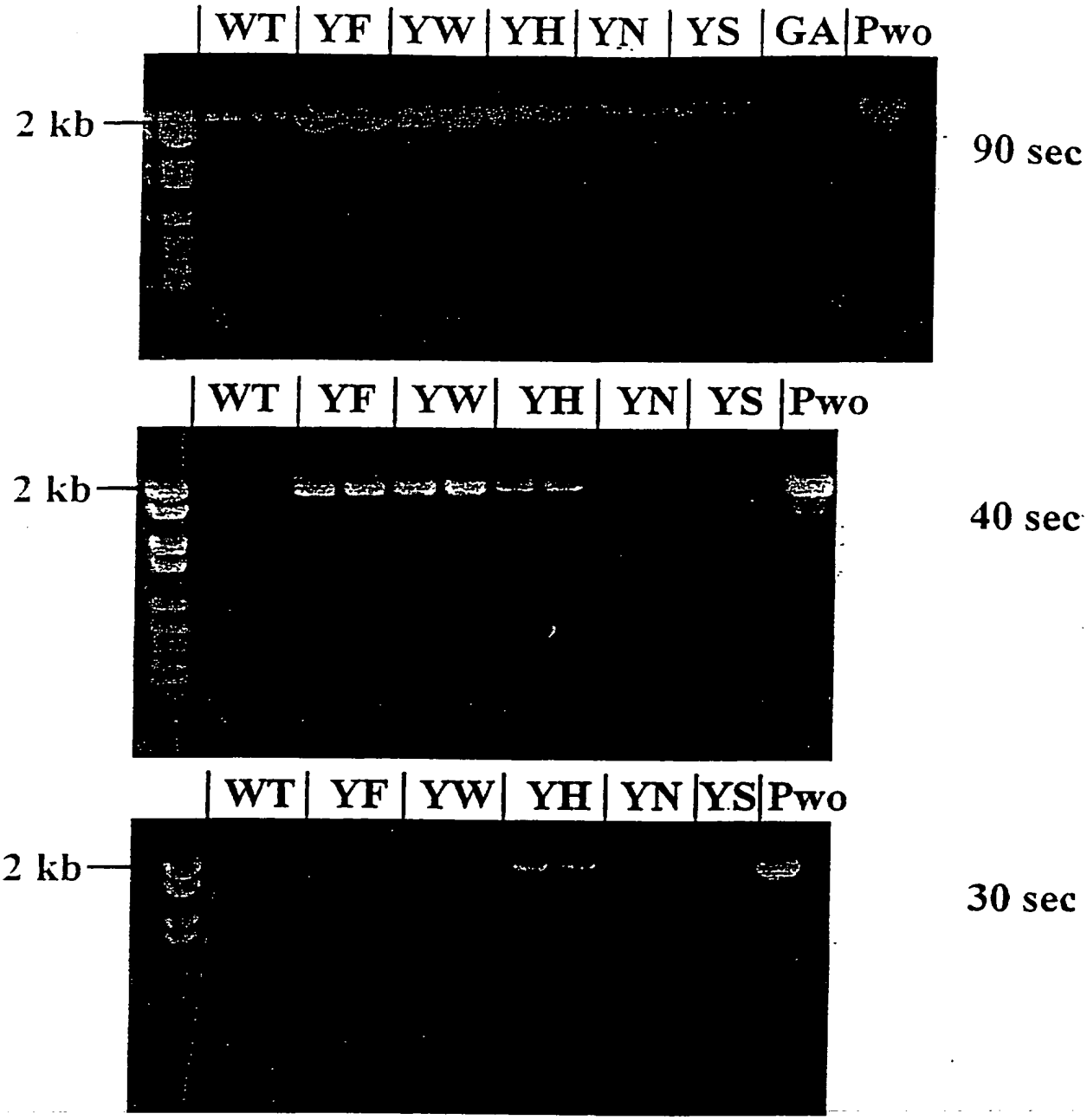

WT YF YW YH YN YS GA Pwo
2 kb
90 sec
WT YF YW YH YN YS Pwo
2 kb
40 sec
WT YF YW YH YN YS Pwo
2 kb
30 sec

Figure 3

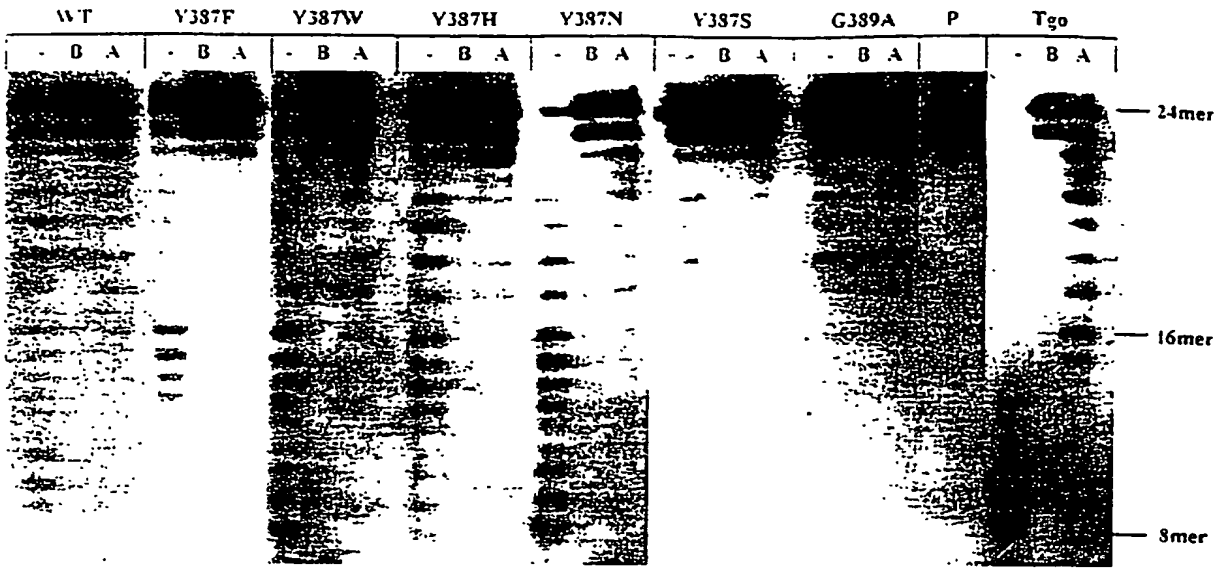

WT
Y387F
Y387W
Y387H
Y387N
Y387S
G389A
P
Tgo
- B A
24mer
16mer
8mer

Figure 4

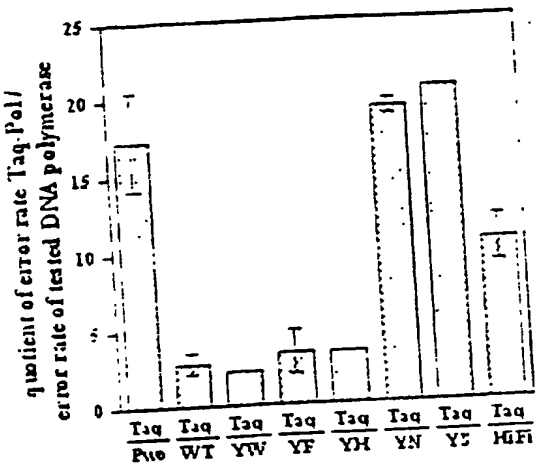
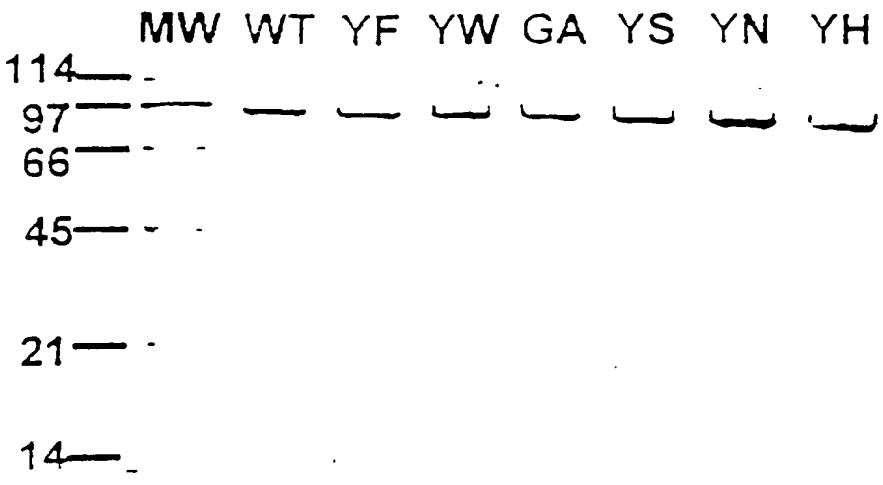

quotient of error rate Taq Pol I/
error rate of tested DNA polymerase
25
20
15
10
0
Taq Pol I
Taq WT
Taq YW
Taq YF
Taq YH
Taq YN
Taq YS
Taq HiFi

Figure 5

Figure 6



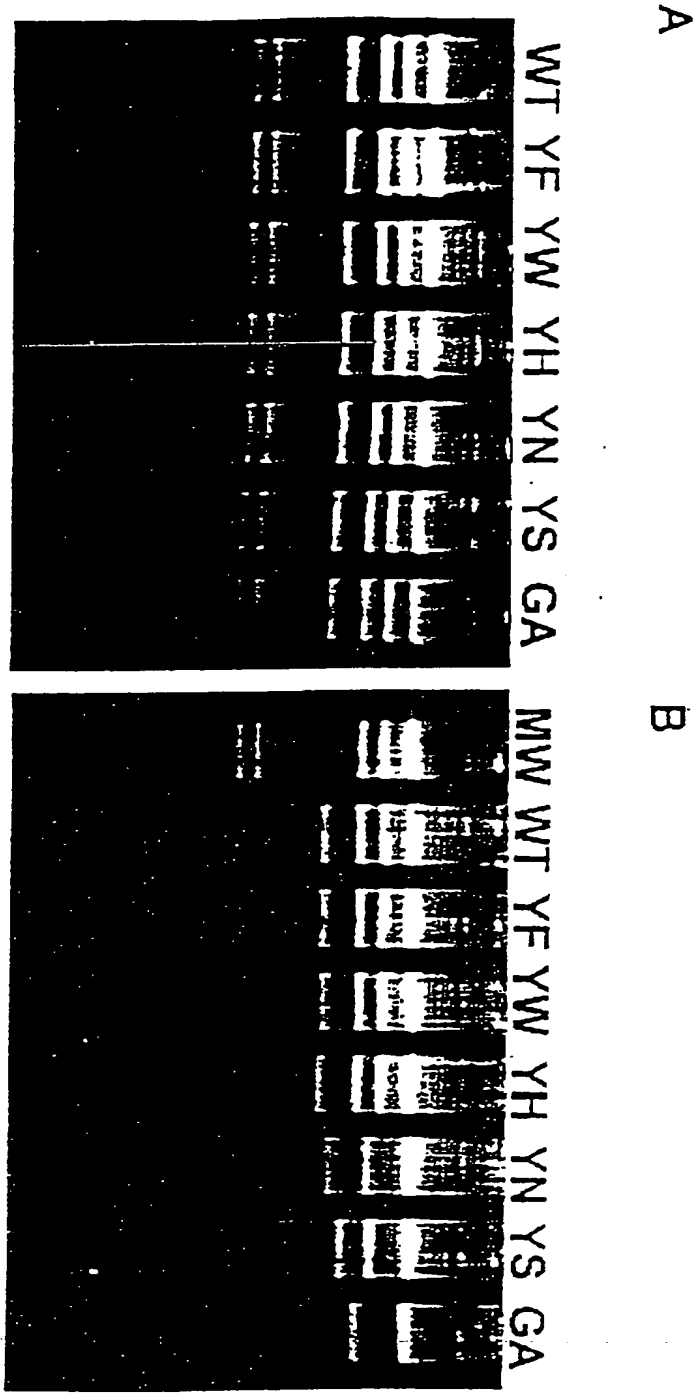


Figure 7

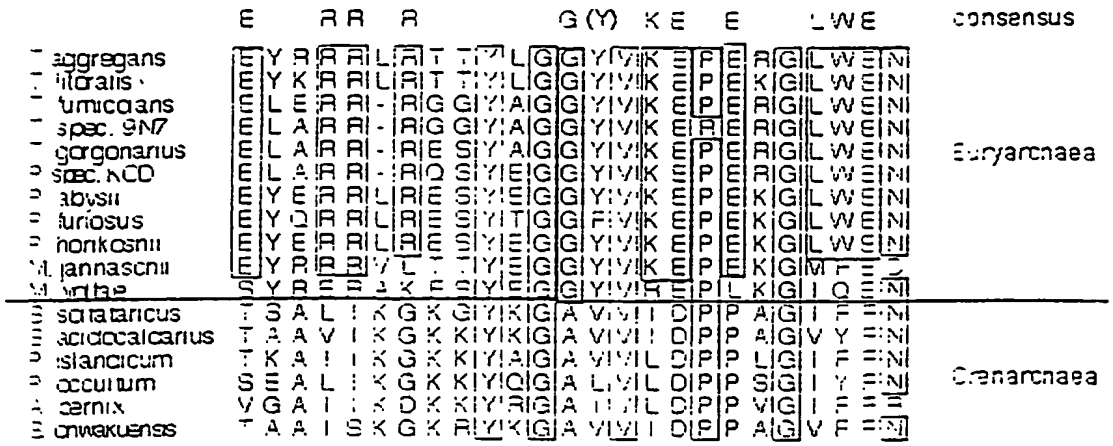


Figure 8

Figure 9/1

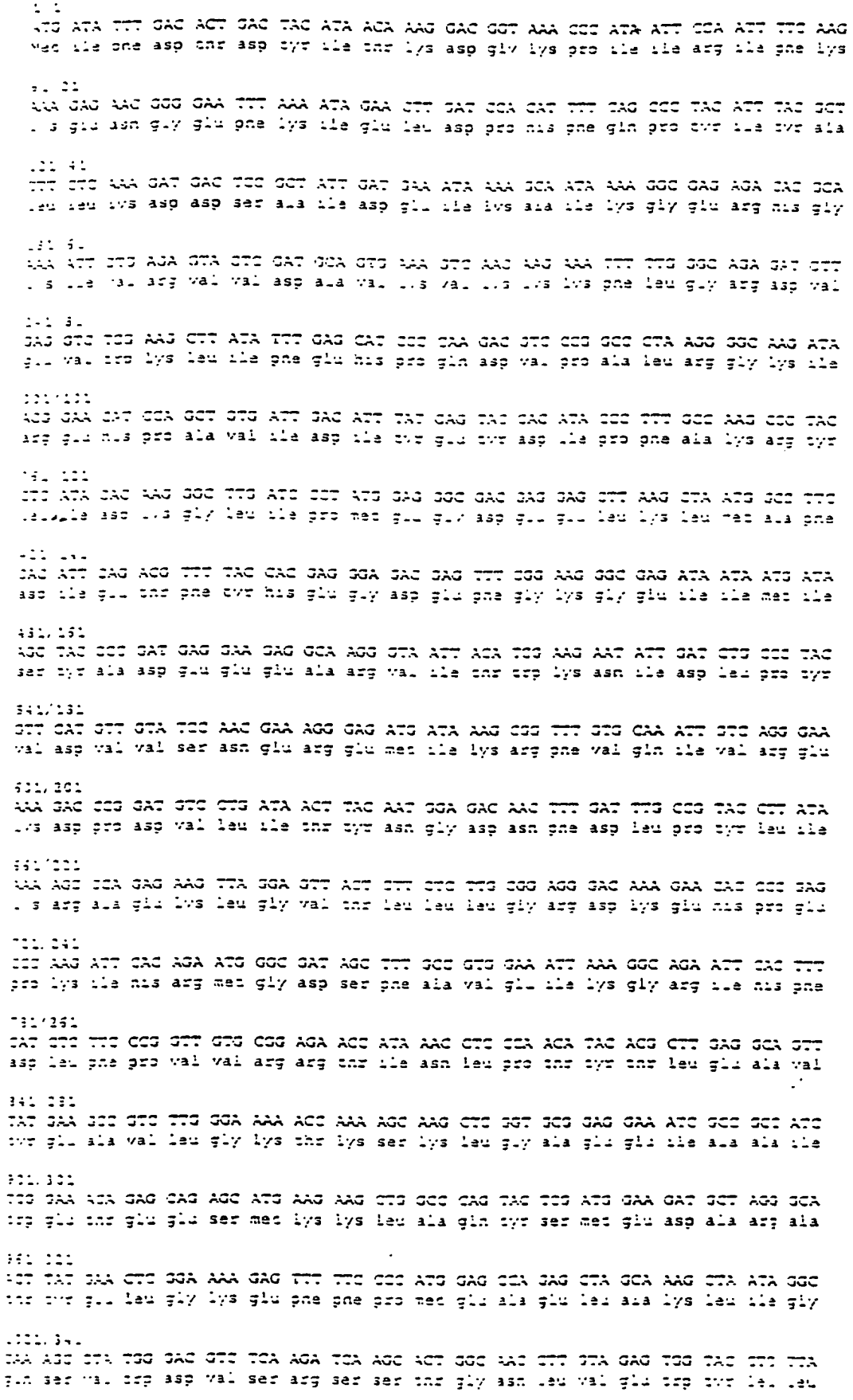

ATG ATA TTT GAC ACT GAC TAC ATA ACA AAG GAC GGT AAA CCC ATA ATT CCA ATT TTC AAG
met ile phe asp thr asp tyr ile thr lys asp gly lys pro ile ile arg ile phe lys
GAA GAG AAC GGG GAA TTT AAA ATA GAA CTT GAT CCA CAT TTT CAG CCC TAC ATT TAC GCT
glu glu asn gly glu phe lys ile glu leu asp pro his phe gln pro tyr ile tyr ala
TTT CTC AAA GAT GAC TCC GCT ATT GAT GAA ATA AAA GCA ATA AAA GGC GAG AGA GAC GCA
leu leu lys asp asp ser ala ile asp glu ile lys ala ile lys gly glu arg his gly
AAA ATT CTG AGA GTA GTC GAT GCA GTG AAA GTC AAC AAG AAA TTT TTG GGC AGA GAT CTT
lys ile leu arg val val asp ala val lys val asn lys lys phe leu gly arg asp val
GAG GTC TCG AAG CTT ATA TTT GAG CAT CCC GAA GAC GTC CCG GCC CTA AGG GGC AAG ATA
glu val ser lys leu ile phe glu his pro glu asp val pro ala leu arg gly lys ile
AGG GAA CAT CCA GCT GTG ATT GAC ACT TAT GAG TAC CAC ATA CCC TTT GCC AAG CCC TAC
arg glu his pro ala val ile asp thr tyr glu tyr asp ile pro phe ala lys arg tyr
CTC ATA CAC AAG GGC TTG ATC CCT ATG GAG GGC GAC GAG GAG CTT AAG CTA ATG GCC TTC
leu ile his lys gly leu ile pro met glu gly asp glu glu leu lys leu met ala phe
GAC ATT GAG ACG TTT TAC CAC GAG GGA GAC GAG TTT CGG AAG GGC GAG ATA ATA ATG ATA
asp ile glu thr phe tyr his glu gly asp glu phe gly lys gly glu ile ile met ile
AGC TAC CCC GAT GAG GAA GAG GCA AGG GTA ATT ACA TGG AAG AAT ATT GAT CTG CCC TAC
ser tyr ala asp glu glu glu ala arg val ile thr trp lys asn ile asp leu pro tyr
GTT GAT GTT GTA TCC AAC GAA AGG GAG ATG ATA AAG CGG TTT GTG CAA ATT GTC AGG GAA
val asp val val ser asn glu arg glu met ile lys arg phe val gln ile val arg glu
AAA GAC CCG GAT GTC CTG ATA ACT TAC AAT GGA GAC AAC TTT GAT TTG CCG TAC GTT ATA
lys asp pro asp val leu ile thr tyr asn gly asp asn phe asp leu pro tyr leu ile
AAA AGC CCA GAG AAG TTA GGA GTT ACT GTT CTC TTG CGG AGG GAC AAA GAA CAC CCC GAG
lys ser pro glu lys leu gly val thr leu leu leu gly arg asp lys glu his pro glu
CCC AAG ATT CAC AGA ATG GGC GAT AGC TTT GCC GTG GAA ATT AAA GGC AGA ATT CAC TTT
pro lys ile his arg met gly asp ser phe ala val glu ile lys gly arg ile his phe
GAT CTC TTC CCG GTT GTG CGG AGA ACC ATA AAC CTC CCA ACA TAC ACG CTT GAG GCA GTT
asp leu phe pro val val arg arg thr ile asn leu pro thr tyr thr leu glu ala val
TAT GAA GCC GTC TTG GGA AAA ACC AAA AGC AAG CTC GGT GCG GAG GAA ATC GCC GCC ATC
tyr glu ala val leu gly lys thr lys ser lys leu gly ala glu glu ile ala ala ile
TGG GAA ACA GAG CAG AGC ATG AAG AAG CTG GCC GAG TAC TCG ATG GAA GAT GCT AGG GCA
trp glu thr glu glu ser met lys lys leu ala glu tyr ser met glu asp ala arg ala
AGT TAT GAA CTC GGA AAA GAG TTT TTC GCC ATG GAG CCA GAG CTA GCA AAG CTA ATA GGC
thr tyr glu leu gly lys glu phe phe pro met glu ala glu leu ala lys leu ile gly
GAA AGC GTA TGG GAC GTC TCA AGA TCA AGC ACT GGC AAC CTT GTA GAG TGG TAC CTC TTA
glu ser val trp asp val ser arg ser ser thr gly asn leu val glu trp tyr leu leu

Figure 9/2

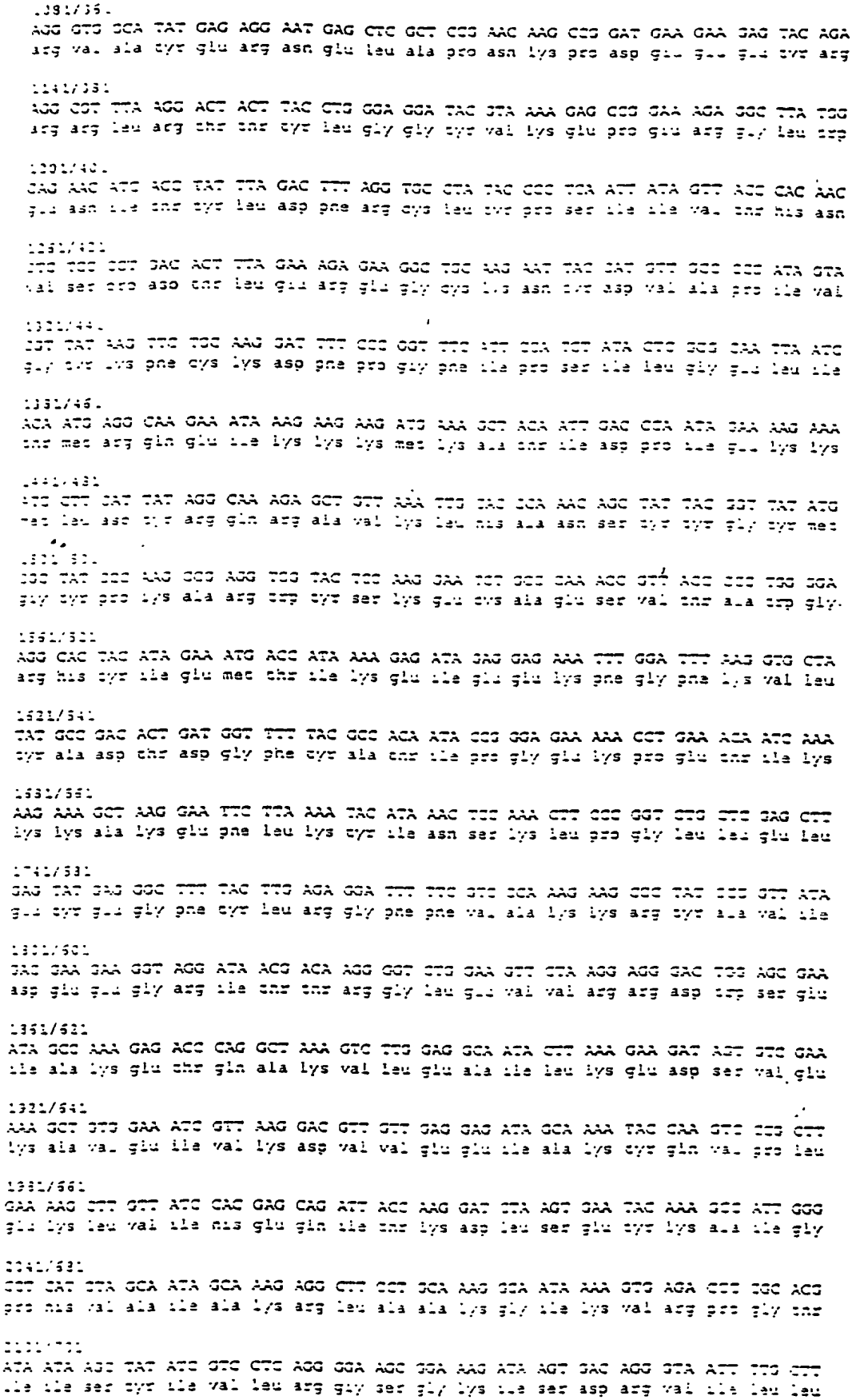
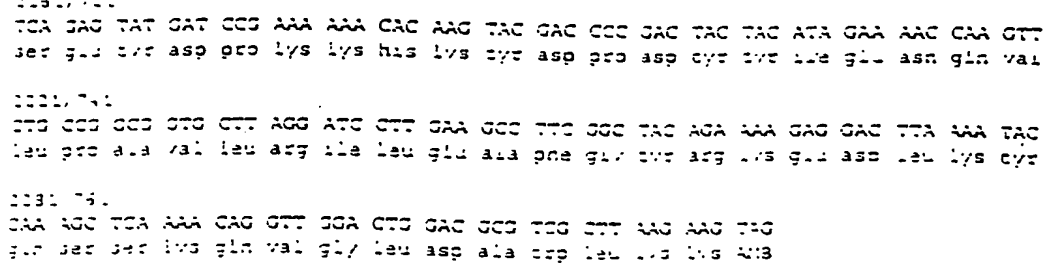

1081/361
AGG GTG GCA TAT GAG AGG AAT GAG CTC GCT CCG AAC AAG CCG GAT GAA GAA GAG TAC AGA
arg val ala tyr glu arg asn glu leu ala pro asn lys pro asp glu glu glu tyr arg
1141/381
AGG CGT TTA AGG ACT ACT TAC CTG GGA GGA TAC GTA AAA GAG CCG GAA AGA GGC TTA TGG
arg arg leu arg thr thr tyr leu gly gly tyr val lys glu pro glu arg gly leu trp
1201/401
GAG AAC ATC ACC TAT TTA GAC TTT AGG TGC CTA TAC CCC TCA ATT ATA GTT ACC CAC AAC
glu asn ile thr tyr leu asp phe arg cys leu tyr pro ser ile ile val thr his asn
1261/421
TTC TCC CCT GAC ACT TTA GAA AGA GAA GGC TGC AAG AAT TAC GAT GTT GCC CCC ATA GTA
val ser pro asp thr leu glu arg glu gly cys lys asn tyr asp val ala pro ile val
1321/441
CGT TAT AAG TTC TGC AAG GAT TTT CCC GGT TTC ATT CCA TCT ATA CTC GCG GAA TTA ATC
gly tyr lys phe cys lys asp phe pro gly phe ile pro ser ile leu gly glu leu ile
1381/461
ACA ATG AGG CAA GAA ATA AAG AAG AAG ATG AAA GCT ACA ATT GAC CCA ATA GAA AAG AAA
thr met arg gln glu ile lys lys lys met lys ala thr ile asp pro ile glu lys lys
1441/481
ATG CTT GAT TAT AGG CAA AGA GCT GTT AAA TTG TAC CCA AAC AGC TAT TAC GGT TAT ATG
met leu asp tyr arg gln arg ala val lys leu his ala asn ser tyr tyr gly tyr met
1501/501
GGC TAT CCC AAG CCG AGG TGG TAC TCC AAG GAA TGT GCC GAA ACC GTT ACC CCC TGG GGA
gly tyr pro lys ala arg trp tyr ser lys glu cys ala glu ser val thr ala trp gly
1561/521
AGG CAC TAC ATA GAA ATG ACC ATA AAA GAG ATA GAG GAG AAA TTT GGA TTT AAG GTG CTA
arg his tyr ile glu met thr ile lys glu ile glu glu lys phe gly phe lys val leu
1621/541
TAT GCC GAC ACT GAT GGT TTT TAC GCC ACA ATA CCG GGA GAA AAA CCT GAA ACA ATC AAA
tyr ala asp thr asp gly phe tyr ala thr ile pro gly glu lys pro glu thr ile lys
1681/561
AAG AAA GCT AAG GAA TTC TTA AAA TAC ATA AAC TCC AAA CTT CCC GGT CTG CTC GAG CTT
lys lys ala lys glu phe leu lys tyr ile asn ser lys leu pro gly leu leu glu leu
1741/581
GAG TAT GAG GGC TTT TAC TTG AGA GGA TTT TTC GTC GCA AAG AAG CCC TAT CCC GTT ATA
glu tyr glu gly phe tyr leu arg gly phe phe val ala lys lys arg tyr ala val ile
1801/601
GAC GAA GAA GGT AGG ATA ACG ACA AGG GGT CTG GAA GTT CTA AGG AGG GAC TGG AGC GAA
asp glu glu gly arg ile thr thr arg gly leu glu val val arg arg asp trp ser glu
1861/621
ATA GCC AAA GAG ACC CAG GCT AAA GTC TTG GAG GCA ATA CTT AAA GAA GAT AGT GTC GAA
ile ala lys glu thr gln ala lys val leu glu ala ile leu lys glu asp ser val glu
1921/641
AAA GCT GTG GAA ACC GTT AAG GAC GTT GTT GAG GAG ATA GCA AAA TAC GAA GTC CCG CTT
lys ala val glu ile val lys asp val val glu glu ile ala lys tyr gln val pro leu
1981/661
GAA AAG CTT GTT ATC CAC GAG CAG ATT ACC AAG GAT CTA AGT GAA TAC AAA GCC ATT GGG
glu lys leu val ile his glu gln ile thr lys asp leu ser glu tyr lys ala ile gly
2041/681
CCT CAT CTA GCA ATA GCA AAG AGG CTT CCT GCA AAG GGA ATA AAA GTG AGA CCC TGC ACG
pro his val ala ile ala lys arg leu ala ala lys gly ile lys val arg pro gly thr
2101/701
ATA ATA AGC TAT ATC GTC CTC AGG GGA AGC GGA AAG ATA AGT GAC AGG GTA ATT TTG CCT
ile ile ser tyr ile val leu arg gly ser gly lys ile ser asp arg val ile leu leu

Figure 9/3


TCA GAG TAT GAT CCG AAA AAA CAC AAG TAC GAC CCC GAC TAC TAC ATA GAA AAC CAA GTT
ser glu tyr asp pro lys lys his lys tyr asp pro asp tyr tyr ile glu asn gln val
CTG CCG GCG GTG CTT AGG ATC GTT GAA GCC TTC GGC TAC AGA AAA GAG GAC TTA AAA TAC
leu pro ala val leu arg ile leu glu ala phe gly tyr arg lys glu asp leu lys tyr
CAA AGC TCA AAA CAG GTT GGA CTG GAC GCG TGG CTT AAG AAG TTG
gln ser ser lys gln val gly leu asp ala trp leu lys lys leu